

#9

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/810,506

DATE: 08/28/2001

TIME: 09:53:58

Input Set : A:\204936US0.txt

Output Set: N:\CRF3\08282001\I810506.raw

ENTERED

3 <110> APPLICANT: TAJI, Teruaki
 4 SHINOZAKI, Kazuo
 5 OHSUMI, Chieko
 7 <120> TITLE OF INVENTION: A METHOD FOR INCREASING STRESS-RESISTANCE TO A PLANT
 9 <130> FILE REFERENCE: 20436US0
 11 <140> CURRENT APPLICATION NUMBER: 09/810,506
 12 <141> CURRENT FILING DATE: 2001-03-19
 14 <150> PRIOR APPLICATION NUMBER: JP2001-072650
 15 <151> PRIOR FILING DATE: 2001-03-14
 17 <160> NUMBER OF SEQ ID NOS: 15
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 344
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Arabidopsis thaliana
 26 <400> SEQUENCE: 1
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 33 20 25 30
 36 Val Thr Phe Leu Ala Gly Asn Gly Asp Tyr Val Lys Gly Val Val Gly
 37 35 40 45
 40 Leu Ala Lys Gly Leu Arg Lys Val Lys Ser Ala Tyr Pro Leu Val Val
 41 50 55 60
 44 Ala Met Leu Pro Asp Val Pro Glu Glu His Arg Arg Ile Leu Val Asp
 45 65 70 75 80
 48 Gln Gly Cys Ile Val Arg Glu Ile Glu Pro Val Tyr Pro Pro Glu Asn
 49 85 90 95
 52 Gln Thr Gln Phe Ala Met Ala Tyr Tyr Val Ile Asn Tyr Ser Lys Leu
 53 100 105 110
 56 Arg Ile Trp Lys Phe Val Glu Tyr Ser Lys Met Ile Tyr Leu Asp Gly
 57 115 120 125
 60 Asp Ile Gln Val Tyr Glu Asn Ile Asp His Leu Phe Asp Leu Pro Asp
 61 130 135 140
 64 Gly Tyr Leu Tyr Ala Val Met Asp Cys Phe Cys Glu Lys Thr Trp Ser
 65 145 150 155 160
 68 His Thr Pro Gln Tyr Lys Ile Arg Tyr Cys Gln Gln Cys Pro Asp Lys
 69 165 170 175
 72 Val Gln Trp Pro Lys Ala Glu Leu Gly Glu Pro Pro Ala Leu Tyr Phe
 73 180 185 190
 76 Asn Ala Gly Met Phe Leu Tyr Glu Pro Asn Leu Glu Thr Tyr Glu Asp
 77 195 200 205
 80 Leu Leu Arg Thr Leu Lys Ile Thr Pro Pro Thr Pro Phe Ala Glu Gln
 81 210 215 220
 84 Asp Phe Leu Asn Met Tyr Phe Lys Lys Ile Tyr Lys Pro Ile Pro Leu
 85 225 230 235 240
 88 Val Tyr Asn Leu Val Leu Ala Met Leu Trp Arg His Pro Glu Asn Val

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89          245          250          255
92 Glu Leu Gly Lys Val Lys Val Val His Tyr Cys Ala Ala Gly Ser Lys
93          260          265          270
96 Pro Trp Arg Tyr Thr Gly Lys Glu Ala Asn Met Glu Arg Glu Asp Ile
97          275          280          285
100 Lys Met Leu Val Lys Lys Trp Trp Asp Ile Tyr Asp Asp Glu Ser Leu
101          290          295          300
104 Asp Tyr Lys Lys Pro Val Thr Val Val Asp Thr Glu Val Asp Leu Val
105 305          310          315          320
108 Asn Leu Lys Pro Phe Ile Thr Ala Leu Thr Glu Ala Gly Arg Leu Asn
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112 Tyr Val Thr Ala Pro Ser Ala Ala
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131 Asp Tyr Val Lys Gly Val Val Gly Leu Ala Lys Gly Leu Arg Lys Ala
132          35          40          45
135 Lys Ser Lys Tyr Pro Leu Val Val Ala Val Leu Pro Asp Val Pro Glu
136          50          55          60
139 Asp His Arg Lys Gln Leu Val Asp Gln Gly Cys Val Val Lys Glu Ile
140 65          70          75          80
143 Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Glu Phe Ala Met Ala Tyr
144          85          90          95
147 Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe Val Glu Tyr
148          100          105          110
151 Asn Lys Met Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe Asp Asn Ile
152          115          120          125
155 Asp His Leu Phe Asp Leu Pro Asn Gly Gln Phe Tyr Ala Val Met Asp
156          130          135          140
159 Cys Phe Cys Glu Lys Thr Trp Ser His Ser Pro Gln Tyr Lys Ile Gly
160 145          150          155          160
163 Tyr Cys Gln Gln Cys Pro Asp Lys Val Thr Trp Pro Glu Ala Lys Leu
164          165          170          175
167 Gly Pro Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val Tyr Glu
168          180          185          190
171 Pro Asn Leu Ser Thr Tyr His Asn Leu Leu Glu Thr Val Lys Ile Val
172          195          200          205
175 Pro Pro Thr Leu Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr Phe Lys
176          210          215          220
179 Asp Ile Tyr Lys Pro Ile Pro Pro Val Tyr Asn Leu Val Leu Ala Met
180 225          230          235          240
183 Leu Trp Arg His Pro Glu Asn Ile Glu Leu Asp Gln Val Lys Val Val

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184                               245                               250                               255
187 His Tyr Cys Ala Ala Gly Ala Lys Pro Trp Arg Phe Thr Gly Glu Glu
188                               260                               265                               270
191 Glu Asn Met Asp Arg Glu Asp Ile Lys Met Leu Val Lys Lys Trp Trp
192                               275                               280                               285
195 Asp Ile Tyr Asn Asp Glu Ser Leu Asp Tyr Lys Asn Val Val Ile Gly
196                               290                               295                               300
199 Asp Ser His Lys Lys Gln Gln Thr Leu Gln Gln Phe Ile Glu Ala Leu
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215 tcaactgccat cagtccaaga cagcgatcga gcttacgtga cgtttcttgc tggaaacggt      120
217 gattacgtga aaggagtcgt tggtttagcc aaaggggttaa ggaaagtcaa atcggccttat      180
219 ccactcgtag tagcgatgtt acccgacgtc ccggagggaac accgtcgtat acttgtggat      240
221 caaggatgca tcgtccgtga aatcgaaccc gtttaccac ccgagaacca aactcagttc      300
223 gccatggctt attacgtcat caactactct aaactccgta tctggaagtt tgtggagtat      360
225 agtaaaatga tatatttaga tggagacatt caagtttacg aaaacatcga tcacttgttt      420
227 gacctaccag atggctatatt gtacgcggtg atggattgtt tctgtgagaa aacatggagt      480
229 cacacgccgc aatacaagat cagatattgc caacaatgcc ccgacaaagt ccagtggcca      540
231 aaagcggagc ttggagagcc accggctctt tacttcaacg ccggaatgtt cttgtacgag      600
233 cctaacctcg agacttacga ggatctacta cgaacactta aaatcactcc tccgactcct      660
235 ttcgctgaac aggatttttt gaacatgtac tttaagaaaa tctacaagcc gattccttta      720
237 gtgtacaatc tcgtccttgc gatgttatgg cgtcacccag aaaatgtaga gcttgaaaaa      780
239 gtcaagggtg ttcactactg tgcagcgggt tcgaagccgt ggagatacac agggaaagaa      840
241 gcgaacatgg agagggaaga tataaaaatg ttagtgaaaa aatggtggga catttacgac      900
243 gacgaatcct tggattacaa gaaacctgtt accgttgttg acacagaggt cgatctcgtg      960
245 aatctgaagc cgttcatcac cgctcttact gaagctggcc ggctcaacta cgtgaccgca     1020
247 ccgtccgctg cttgaatgtt gccaggagtt aaaattgtcg gtgg                               1064
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251 <211> LENGTH: 29
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: synthetic DNA
258 <400> SEQUENCE: 4
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262 <210> SEQ ID NO: 5
263 <211> LENGTH: 29
264 <212> TYPE: DNA
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271 caaggatccc ctggcaatca agcagcgga	29
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276 <212> TYPE: DNA	
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279 <220> FEATURE:	
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283 cgccacagta caagatcggt ta	22
286 <210> SEQ ID NO: 7	
287 <211> LENGTH: 20	
288 <212> TYPE: DNA	
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291 <220> FEATURE:	
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294 <400> SEQUENCE: 7	
295 catgaagagg cgtatgcagc	20
298 <210> SEQ ID NO: 8	
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301 <213> ORGANISM: Artificial Sequence	
303 <220> FEATURE:	
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306 <400> SEQUENCE: 8	
307 ctttctcggga caagatggca	20
310 <210> SEQ ID NO: 9	
311 <211> LENGTH: 20	
312 <212> TYPE: DNA	
313 <213> ORGANISM: Artificial Sequence	
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319 gtgttgacaa gaacctcgct	20
322 <210> SEQ ID NO: 10	
323 <211> LENGTH: 32	
324 <212> TYPE: DNA	
325 <213> ORGANISM: Artificial Sequence	
327 <220> FEATURE:	
328 <223> OTHER INFORMATION: synthetic DNA	
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335 <211> LENGTH: 32	
336 <212> TYPE: DNA	
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355 cgcggatcca tggcacctga gatcaatacc 30
358 <210> SEQ ID NO: 13
359 <211> LENGTH: 30
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
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364 <223> OTHER INFORMATION: synthetic DNA
366 <400> SEQUENCE: 13
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371 <211> LENGTH: 36
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial Sequence
375 <220> FEATURE:
376 <223> OTHER INFORMATION: synthetic DNA
378 <400> SEQUENCE: 14
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385 <213> ORGANISM: Artificial Sequence
387 <220> FEATURE:
388 <223> OTHER INFORMATION: synthetic DNA
390 <400> SEQUENCE: 15
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/810,506

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Input Set : A:\204936US0.txt

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